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ABSTRACT

The purpose of the research was to manipulate two aspects of genetics instruction in order to measure their effects on college, introductory biology students' achievement in genetics. One instructional sequence that was used dealt first with monohybrid autosomal inheritance patterns, then sex-linkage. The alternate sequence was the reverse. Instruction was individually delivered via microcomputer tutorials to 41 engineering and science majors enrolled in a Purdue University introductory biology course. Computer delivered instruction was chosen to control for teacher effects. In terms of achievement the average score of the subjects who received integrated instruction was significantly higher than that of those who received the non-integrated instruction. Also, the groups which received integrated presentations scored significantly higher on two novel genetics problems that required a meaningful understanding of the role of meiosis in genetic inheritance. (Author/TW)

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ABSTRACT

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The purpose of the research was to manipulate two aspects of genetics instruction in order to measure their effects on college, introductory biology students achievement in genetics.

The study was conducted as a true experiment and utilized a fully randomized 2 X 2 factorial design. One independent variable was the degree to which meiosis was instructionally integrated with genetics. At one level of integration, meiosis was treated separately from genetic inheritance. At the other level, meiosis was used in genetics contexts to explain the results of gametogenesis. The other independent variable was instructional sequence. One sequence, similar to that found in many biology texts, dealt first with monohybrid autosomal inheritance patterns, then sex-linkage. The alternate sequence, suggested by R. R. Tolman, was the reverse.

Instruction was individually delivered via microcomputer tutorials to 41 engineering and science majors enrolled in a Purdue University introductory biology course. Computer delivered instruction was chosen to control for teacher effects.

The criterion test was developed by the investigator and measured a subject's ability to define genetics terms, state relationships between terms, and solve various types of familiar and novel genetics problems.

A two-way ANOVA of the scores from each of the ten test tasks and the total test score revealed the following. In terms of the test overall, the

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average score of the subjects who received integrated instruction was significantly higher than that of those who received the non-integrated instruction. With respect to the individual test tasks, the Tolman sequence groups scored significantly higher on the definitions task than did the non-Tolman groups. However, the non-Tolman groups scored significantly higher on the monohybrid genetics problem. Finally, the groups which received integrated presentations scored significantly higher on two novel genetics problems that required a meaningful understanding of the role of meiosis in genetic inheritance.

In terms of genetics instruction, these results favor the integrated approach. However, the sequence results are less clear, providing conflicting evidence as to the general efficacy of the alternate approaches.

The Effects of Meiosis/Genetics Integration and Instructional Sequence on College Biology Students' Achievement in Genetics

Paper presented at the
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INTRODUCTION

The principles of genetics are both fascinating and powerful in that they not only explain inheritance, but also interrelate the structures, the functions and the evolution of living organisms. Biology educators have long been aware of the power of genetic principles to explain and organize data, and thus many have recognized the importance of genetics in biology curricula, as was recently indicated by Finley, Stewart and Yarroch (1982). Although important to well-rounded biology courses, genetics and its related topics have been rated by teachers and students to be among the most difficult content to learn (Finley et al.; Johnstone & Mahmoud, 1980), and the problems students experience with genetics are legion (Hildebrand, 1985). One such problem that has recently been the focus of research involves the failure of students to appreciate the relationship between meiosis and genetics.

The failure of some students to recognize the vital role that meiosis plays in a study of inheritance has been well documented. For example, in two studies Stewart (1982, 1983) utilized tape-recorded, think-aloud, problem solving sessions with a total of 41 high school biology students to gather data on their genetics problem solving strategies. One major finding of both studies was that some subjects could successfully solve genetics problems without adequate knowledge of the meiosis-inheritance link. However, Stewart concluded that the problem solving was not meaningful because the students could not explain, in biological terms, the origin of the parental gametes.

Tolman (1982) also used the taped interview technique in his work with 30 high school students who had completed tenth-grade biology. He found that some of his subjects had difficulty solving monohybrid and codominance problems because they did not properly assign alleles to gametes. Tolman

claimed that the difficulties would have been avoided if the students were more aware of the movements of chromosomes and alleles during the first meiotic division.

The problem of relating meiosis to genetics is not solely one of high school students, as was shown by Peard (1983), who studied 40 Cornell introductory biology students. Using interviews to assess their previous genetics instruction, Peard found that 17 of them saw no connection between meiosis and genetics problem solving. The remainder were aware of the relationship, but only three could remember meiosis, and those three could not clearly state the relationship.

Finally, Browning and Lehman (in press) used microcomputer programs to gather data concerning the genetics misconceptions of 135 college, introductory biology students. They found the assignment of alleles to gametes in simple genetics problems to be a significant stumbling block for a number of the students. Many of the gamete errors indicated a lack of knowledge concerning how alleles segregate and assort in meiosis.

In conclusion, several investigators who used different data gathering techniques and who studied various kinds of biology students have discovered an important missing conceptual link between meiosis and genetics. In some cases, the missing link apparently made it difficult for students to solve genetics problems; in others, the missing link undermined their meaningful solution.

After the missing conceptual link was elucidated, educational researchers began to propose methods for meaningfully integrating meiosis and genetics. Recently, Lehman (1988) made a modest attempt to integrate meiosis and genetics in the biology curriculum of preservice elementary school teachers attending Purdue University. Lehman's study had a media focus and

tried to assess the impact of computer-based activities on the preservice teachers' biology achievement, as well as their attitudes toward biology and computers. A small segment of his study incorporated a microcomputer-based genetics problem solving tutor which interacted with subjects as they attempted to solve two monohybrid and two dihybrid problems. The program was able to detect when a subject was having difficulty completing any one of the several steps required to solve the genetics problems. When a subject failed to properly assign alleles to gametes, the program presented a meiosis-based tutorial which explained the allele sorting process. Of Lehman's 187 subjects, 97 interacted with the program, and the others were simply given time to practice genetics problem solving on their own with some assistance from their instructors. The subjects then wrote a "genetics paper" in which they proposed a model of inheritance based upon their own Drosophila experiments and other lab activities, which for some included use of the tutoring program. Using that criterion, Lehman found no particular achievement difference between the two groups. He attributed this outcome to a lack of sensitivity on the part of the measures used to gauge achievement.

Using a more direct approach, Allen and Moll (1986) have instituted classroom instructional procedures and special homework exercises which were designed to reinforce the meiosis/genetics link for college, introductory biology students. In the Allen and Moll curriculum, use of the Punnett square algorithm was replaced by diagrams of meiosis and fertilization which emphasized gene-chromosome relationships. Also, full credit on genetics homework could only be earned by use of the meiotic approach. Moll and Allen (1987) reported that students who used the integrated or meiosis-based approach on monohybrid genetics problems were more likely than the students who used an algorithmic method to solve the problems successfully. However,

these are not experimental results because all subjects received the integrated instruction. Therefore, it may be that the successful problem solvers were more likely to choose the somewhat more complex meiotic approach, and the less successful students were more likely to utilize the simpler, algorithmic method.

Thomson and Stewart (1985) made recommendations as to how to structure a curriculum which would make the relationship between genetics and meiosis less mysterious. Their suggestions included a simplification of meiosis vocabulary, a greater emphasis on the relationship between genes and chromosomes, an increase in the number and quality of text diagrams of meiosis, and consistent use of the terms gene, allele and trait. These two investigators did not report the effects of their suggestions on student performance.

Cho, Kahle and Nordland (1985) proposed a number of teaching strategies aimed at improving genetics instruction. Their suggestions with respect to meiosis/genetics integration were theoretical and sequence-based. They argued that the assimilation theory of Ausubel, Novak and Hanesian (1978) suggests a sequence which should begin with genetics, flow to meiosis and then finish with chromosome theory. Cho, Kahle and Nordland claimed that such a sequence would promote the desired conceptual linkage via subsumption, but they did not actually conduct a study to assess the effects of the proposed sequence.

Finally, Tolman (1982) also published an instructional approach designed to integrate the ideas of meiosis with those of genetics. Tolman outlined and called for an evaluation of a specific scope and sequence of genetics instruction that was different from what he termed the traditional approach (see Figure 1). Tolman's suggestions are worth examining in some

Traditional	Tolman
Meiosis (no genes on chromosomes)	Meiosis (genes on chromosomes)
Mendel's Pea Experiments (Introduce basic genetic vocabulary and inheritance model)	Sex Chromosomes in Humans (show genes on chromosomes and trace back to meiosis)
Monohybrid Cross (autosomal)	Sex-linked Traits in Humans (emphasize meiosis and introduce basic genetic vocabulary and inheritance model)
Dihybrid Cross	Monohybrid Cross
Incomplete Dominance (Codominance)	Dihybrid Cross (autosomal and in humans)
Sex Chromosomes	Codominance (in humans)
Sex Determination	Mendel's Pea Experiments
Sex-linked Traits	

Figure 1
Traditional and Tolman Genetics Curricula, Modified from Tolman (1982)

detail because they were the basis for the instructional independent variables used in this study.

Tolman's (1982) suggested curriculum was different from the traditional in three ways. First, Tolman focused on human inheritance, rather than that of fruit flies or garden peas. Although a human-centered approach has motivational value, Tolman chose it because it allowed his curriculum to begin genetics with information concerning human sex chromosomes and sex determination that he argued was already present in the cognitive structures of novice genetics students. Such a beginning naturally led to the next difference between the two curricula: topical sequence. Tolman's sequence began with sex-linkage and then moved on to autosomal patterns of inheritance. In contrast, many biology textbooks follow the reverse order (Browning, 1987). Also, because textbooks heavily influence curricula at the high school and introductory college levels (Hurd, Bybee, Kahle, & Yager, 1980; McInerney, 1986; Wivagg, 1987), many biology courses probably follow an instructional sequence similar to what Tolman called traditional. Finally, Tolman's approach emphasized the gene-chromosome relationship and drew meiosis into the discussion of genetic inheritance; thus Tolman's curriculum was integrated, as well as human-centered and based upon a non-standard sequence.

The explicit nature of Tolman's curriculum suggestions and his request for a well controlled test of them provided the motivation for the implementation of an experiment to evaluate his ideas. However, the simultaneous evaluation of three binary instructional variables was a problem. A factorial experiment which manipulated all three variables would require eight treatment groups and at least 80 subjects. Because that many subjects were not available, it was decided to test only the integration and sequence variables while using human genetic inheritance in all treatments.

In summary, a review of the relevant literature revealed that some genetics students did not appreciate the link between meiosis and genetic inheritance. Some of these students had trouble solving and/or justifying their solutions to genetics problems. Among others, Tolman (1982) suggested an instructional approach designed to relieve some of the students' difficulties. The study described below is an examination of the effects of two of Tolman's suggestions on college, introductory biology students' achievement in genetics.

METHODOLOGY

Design

The study utilized a 2 X 2 fully randomized, factorial, experimental design with each independent variable at two, fixed levels. One independent variable was meiosis/genetics integration in which either meiotic or algorithmic approaches to gametogenesis were taught. The other independent variable was topical sequence. One sequence, which was devised by Tolman (1982), discussed single gene pair sex-linkage first, then monohybrid autosomal inheritance; the other, which conformed to that found in most biology texts, was the reverse. The various combinations of independent variables and the resulting treatment groups are summarized in Figure 2.

Subjects

The 41 subjects represented the entire enrollment of an introductory biology course held at Purdue University during the fall of 1986. Each subject provided information concerning his/her age, gender, school major and SAT scores. This information was elicited and recorded by the computer program which subsequently delivered the instructional treatment. The

Sequence	Level of Integration: Integrated	Level of Integration: Non-Integrated
Tolman-like	Group 1	Group 3
Non-Tolman (traditional)	Group 2	Group 4

Figure 2
Experimental Design Layout

subjects were generally engineering and science majors, as indicated in Table 1. The four treatment groups, to which the subjects were individually and randomly assigned, are characterized in Table 2.

As indicated above, the SAT data were collected via student self-report. Although it may seem risky to rely on self-reports, Hamilton (1981) found moderate to high (0.70 to 0.90) correlations between college student self-report of SAT scores and the objective measures. The SAT data were gathered to determine if, at least by these measures of scholastic ability, the treatment groups were different before the experiment began. A one-way ANOVA of the SAT verbal and math scores detected no significant differences, as is shown in Tables 3 and 4.

Treatments

Computer-Delivered Tutorials

Because it was feared that the effects of the instructional variables would be obscured by natural fluctuations in teacher performance, the four treatments were prepared solely by the investigator and then incorporated into separate computer programs. The use of instructional software guaranteed that a given treatment could be reliably repeated and the different treatments would vary only as prescribed by the investigator.

Each computer program was a tutorial which consisted of a series of screens that displayed text, graphics, animations, and multiple-choice questions designed to facilitate the learning of certain introductory genetics terms, concepts and rules (see Table 5). The programming was done in Borland's Turbo Pascal environment (Borland International, 1985).

In general, the tutorials utilized white text and high-resolution graphics on a black background and were user-friendly. The text was 80-column, double-spaced and non-scrolling to enhance reading efficiency and

Table 1
Student Majors

Major	Percent (n=41)
Engineering	34
Chemistry	30
Math	10
Health (pre-med,etc)	7
Other (psychology, geoscience,etc)	19

Table 2
Characteristics of Treatment Groups

	Group			
Characteristic	1	2	3	4
Number of Subjects	9	10	11	11
Gender				
Female	7	3	5	4
Male	2	7	6	7
Age (yrs.)				
Average	19.7	21.4	20.5	20.4
SD	1.1	1.8	1.2	1.0
SAT Verbal				
Average	575.7	519.0	606.3	565.0
SD	78.1	114.6	35.8	59.9
SAT Math				
Average	625.7	682.0	666.3	626.1
SD	102.6	61.8	46.9	85.4

Table 3
One-way ANOVA of Self-report SAT Verbal Scores

Source	df	SS	MS	F	p
Groups	3	35489.6	11829.9	1.87	0.1552
Error	31	196098.9	6325.8		

Table 4
One-way ANOVA of Self-report SAT Math Scores

Source	df	SS	MS	F	p
Groups	3	22145.1	7381.7	1.28	0.2980
Error	31	178567.8	5670.3		

Table 5
Tutorial Characteristics

Characteristic	Tutorial 1	2	3	4
Number of Screens	247	252	229	232
Number of Graphics	141	141	125	125
Number of Animations	7	7	5	5
Number of Questions	75	75	74	74
Fry (1968,1977) Reading Grade Level	8	9	9	8

comprehension (Kolers, Duchnicky, & Ferguson, 1981; Oleron & Tardieu, 1978). The text was complemented by simple graphics which represented chromosomes and cells. The user controlled the screen presentation rate and had the option of reviewing earlier screens. Also, due to the length of the tutorials, subjects were able to quit at any time and then return later to resume work where they left off.

The instructional software was run on Zenith (IBM compatible) microcomputers. Each subject interacted individually with his or her tutorial via a 96-character keyboard and viewed output on a CRT monitor.

Independent Variables

One independent variable was the extent to which discussions of meiosis were integrated with those of genetic inheritance. The critical features of the integration variable may be found in Figure 3. In terms of integration, item #1 of Figure 3 emphasized the relationship between genes and chromosomes and showed that the movements of genes and chromosomes in meiosis are correlated. On the other hand, the non-integrated tutorials focused only on the chromosome movements. Item #2 of the integrated tutorials showed the subjects how meiosis could be useful in determining parental gametes in genetic contexts and emphasized the importance of biological justifications for the steps taken in the solution of genetics problems. One consequence of item #2 was that meiosis was repeated in genetic contexts several times, once for each different pattern of inheritance. Another consequence was that the integrated tutorials (numbers 1 and 2 in Table 5) had more screens, graphics, animations, and questions than did the non-integrated tutorials (numbers 3 and 4 in Table 5). It simply took more text, graphics, animations, and questions to explain the role of meiosis in each inheritance pattern than to use a

Integrated	Non-integrated
1) Showed genes on chromosomes in meiosis.	1) Did not show genes on chromosomes in meiosis.
2) In the context of genetic inheritance, meiosis was used to determine the genetic compositions of the parental gametes.	2) In genetic contexts, a Mendelian algorithm was used to determine the genetic compositions of parental gametes.
3) Emphasis was placed on the biological meanings of the Punnett square symbology.	3) No emphasis on the biological meanings of the Punnett square symbology.

Figure 3
Description of the Two Levels of Integration

Mendelian algorithm to generate the parental gametes. (The Mendelian algorithm was a rule which dictated that each gamete should contain only one allele from each pair found in a diploid cell.) The final element of integration was the symbology associated with the Punnett square. In the integrated tutorials the biological meanings of the symbols were stressed, especially the origin of the gamete symbols. The emphasis placed on the meanings of the symbols was designed to undermine the rote use of the Punnett square. Algorithmic use of the square can be detrimental to the understanding of the role of meiosis in genetic inheritance (Fisher et al., 1986; Longden, 1982; Stewart, 1982).

Integration was not the only difference between the tutorials; instructional sequence, as outlined in Figure 4, was another. In keeping with the experimental design, tutorials 1 and 3 utilized a Tolman-like sequence, while tutorials 2 and 4 conformed to an approach inspired by the traditional sequence shown in Figure 1. Tutorials 2 and 4 did differ slightly from the sequence shown in Figure 1 in that dihybrid inheritance was discussed <u>after</u> sex-linkage. This was done so that the two sequences would differ in only <u>one</u> respect, i.e. when sex-linkage was presented.

The initial portions of the tutorials began with a module which introduced the subject matter and developed a rationale for studying genetic inheritance in humans. The next module listed instructions for using the tutorial, how to quit, and provided a reminder for the upcoming criterion test.

Following the instructions was a module which introduced chromosomes. This module described chromosome structure, function and location. It also established the relationship between genes and chromosomes and defined the term homologue.

Tutorial 1	Tutorial 2	Tutorial 3	Tutorial 4
Introduction	Introduction	Introduction	Introduction
Instructions	Instructions	Instructions	Instructions
Chromosomes	Chromosomes	Chromosomes	Chromosomes
Meiosis	Meiosis	Meiosis	Meiosis
Genetic model introduced (Hemophilia)	Genetic model introduced (Huntington's Disease)	Genetic model introduced (Hemophilia)	Genetic model introduced (Huntington's Disease)
Hemophilia inheritance	Huntington's inheritance	Hemophilia inheritance	Huntington's inheritance
Color-blindness inheritance	Rh blood type inheritance	Color-blindness inheritance	Rh blood type inheritance
Huntington's inheritance	Cystic fibrosis inheritance	Huntington's inheritance	Cystic fibrosis inheritance
Rh blood type inheritance	Hemophilia introduction	Rh blood type inheritance	Hemophilia introduction
Cystic fibrosis inheritance	Hemophilia inheritance	Cystic fibrosis inheritance	Hemophilia inheritance
Beta-Thal. & Rh intro. (Dihybrids)	Color-blindness inheritance	Dihybrid Meiosis	Color-blindness inheritance

Figure 4
Topical Sequence of the Tutorials

Tutorial 1	Tutorial 2	Tutorial 3	Tutorial 4
Beta-Thal. & Rh gameto-genesis	Beta-Thal. & Rh intro (Dihybrids)	Beta-Thal. & Rh intro (Dihybrids)	Dihybrid Meiosis
Beta-Thal. & Rh zygotes	Beta-Thal. & Rh gameto-genesis	Beta-Thal. & Rh inheritance	Beta-Thal. & Rh intro (Dihybrids)
Cystic fib. & Huntington's intro & gametes	Beta-Thal. & Rh zygotes	Cystic fib. & Huntington's intro & gametes	Beta-Thal. & Rh inheritance
Cystic fib. & Huntington's zygotes	Cystic fib. & Huntington's intro & gametes	Cystic fib. & Huntington's zygotes	Cystic fib. & Huntington's intro & gametes
	Cystic fib. & Huntington's zygotes		Cystic fib. & Huntington's zygotes

Figure 4, continued

Once the chromosome concepts were established, the tutorials then discussed meiosis. The movements of a single pair of chromosomes in meiosis were emphasized with animated graphics. Meiosis was reviewed using a 'meiosis construction kit' in which the subjects were presented with the 'cells' and 'chromosomes' of meiosis and were asked to arrange the 'chromosomes' as they would appear in the various stages of the division process. Also, one screen near the end of the meiosis module of each tutorial discussed the phenomenon of non-disjunction.

After meiosis, the tutorials introduced a model of monohybrid inheritance which was modified from Mendel. The features of this model were: (a) a pair of alleles control the expression of a given trait, (b) one allele of the pair comes from the mother and the other from the father, and (c) genes exist in two forms: either dominant or recessive. Although the model was introduced at the same point in all tutorials, the context of the introduction varied as was dictated by the differences in sequence. In the Tolman-like sequences (tutorials 1 and 3 of Figure 4) the model was introduced against the background of a sex-linked disease called hemophilia. In the non-Tolman sequences (tutorials 2 and 4), Huntington's Disease, a neurological disorder inherited in the autosomal dominant pattern, provided the matrix for the model. Once the model was introduced, an example of inheritance using the model was discussed. The example first showed and explained the parental genotypes, showed how the genetic compositions of the parental gametes could be determined, described the use of the Punnett square, discussed the possible zygotes, and then quizzed the subjects concerning the concepts of inheritance encountered up to that point. This same pattern was repeated with small variations for the remainder of the monohybrid portion of the tutorials. In general, hemophilia and color blindness were given as examples of sex-linked

inheritance, Huntington's Disease and Rh blood type as examples of the autosomal dominant pattern and cystic fibrosis as an example of the autosomal recessive pattern.

In contrast to the single gene pair orientation of the inheritance patterns described above, the last portions of the tutorials concentrated on the simultaneous inheritance of two gene pairs. In this dihybrid section the sequence was virtually the same for all tutorials. However, the non-integrated tutorials required a short digression into meiosis with two chromosome pairs before beginning the beta-thalassemia and Rh inheritance discussion. In all tutorials, beta-thalassemia required the introduction of concepts relating to hemoglobin. Then the discussion of the simultaneous inheritance of beta-thalassemia and Rh blood type began with the establishment of the parental genotypes and continued as outlined above with the monohybrids. The final sections of the tutorials explored the dihybrid inheritance of cystic fibrosis and Huntington's Disease.

Implementation of Treatment

The study was conducted during the last two weeks of September 1986, and was completed before the subjects encountered meiosis and genetics in their regular coursework. Subjects individually interacted with the tutorials during two regularly scheduled lab periods. As indicated in Table 6, the subjects using the integrated tutorials (1 and 2) required more time to finish than the others, but this difference is not statistically significant, as is shown in Table 7.

Table 6
Average Completion Times

Group	Average Time (min.)	SD
1	149.6	41.3
2	146.1	40.2
3	122.3	36.9
4	130.4	36.2

Table 7
One-way ANOVA of Completion Times

Source	df	SS	MS	F	p
Groups	3	5093.7	1697.9	1.14	0.3440
Error	37	54905.9	1483.9		

The Criterion Test and Dependent Variables

The general research question was how the instructional variables affected college, introductory biology students' achievement in genetics. Objective measures of that achievement were obtained using test questions devised by the investigator. Using the research of Stewart (1983) as a guide, monohybrid and dihybrid inheritance problems were devised which asked subjects to determine the genetic composition of the parental gametes, and the zygotic genotypes, phenotypes and phenotypic ratios. A trihybrid problem was also included, but it simply asked for the genetic composition of the gametes of one parent. Within the monohybrid, dihybrid and trihybrid problems were "integration tasks", which asked subjects to justify their assignment of alleles to gametes. Additionally, the integration construct was further measured by two questions which focused on meiotic anomalies. One question presented a gamete that contained two alleles from the same pair. Subjects were asked whether such a gamete was possible and to justify their answers. The other involved a dihybrid parent in which the homologues of one chromosome pair fail to separate in the first meiosis. The students were asked to predict the genetic composition of the resulting gametes. Finally, to more fully gauge achievement, the subjects were also presented with a concept relations task. The task required a subject to state a relationship between two terms and also define the terms. In all, ten criterion tasks were devised, and the dependent variables consisted of the overall test score and the score on each of the ten tasks. The criterion test and scoring key may be found in Appendix A, and the overall test structure is outlined in Table 8.

The test was given to all subjects at the same time during a regularly scheduled 50-minute lecture period approximately one week after the end of the tutorials. The subjects were informed of the test in advance and knew it was

Table 8
Point Values for the Criterion Test Questions

Division/Components	Point Value
Genetics Problems/	41
Monohybrid Autosomal Inheritance	16
Dihybrid Autosomal Inheritance	23
Trihybrid Gamete	2
Integration Tasks/	24
Monohybrid Gamete Justification	4
Dihybrid Gamete Justification	4
Trihybrid Gamete Justification	4
Meiotic Anomaly-Aneuploid Gamete	4
Meiotic Anomaly-Dihybrid Non-Disjunction	8
Concept Relations Task/	18
Definitions	10
Relationships	8
Total	41+24+18 = 83

worth about 10% of their final grades.

All tests were scored by the investigator. The tests were given code numbers so as to conceal the identity of the subjects during grading. Finally, the internal consistency reliability (Cronbach's alpha) of the criterion test was 0.6401.

RESULTS AND DISCUSSION

The data collected on each dependent variable was subjected to a two-way analysis of variance. Because of unequal cell size, all ANOVA's were calculated using general linear procedures, and F probabilities less than 0.05 were considered significant. Finally, because no significant interaction between independent variables was detected, the impact of each is presented separately.

As indicated in Table 8, the criterion test was worth 83 points. The average test score across all groups was 58.54 with a standard deviation of 10.11 and a range of 38 to 76.

Integration Variable

It was expected that the integrated approach to teaching meiosis and genetics would promote better performance on the "integration tasks" shown in Table 8, and, in turn, perhaps affect the total test scores. The impact of the integrated approach on the other measures of achievement was difficult to predict, but its rather narrow focus made it unlikely to significantly affect the scores of the "genetics problems" and the "concept relations task" outlined in Table 8.

Not unexpectedly, the overall test scores were affected by the integration instructional variable, as is shown in the first line of Table 9.

Table 9
Summary of ANOVA Results and Means for INTEGRATION VARIABLE

TASK	MS	F(1,37)	p	MEANS (I/NI)
Test Overall	450.95	4.67	0.0372*	62.1/55.5
Trihybrid Justification	13.95	7.58	0.0091**	1.6/0.4
Trihybrid Gametes	0.06	0.20	0.6547	1.9/1.8
Aneuploid Gamete	3.47	4.48	0.0411*	0.95/0.36
Dihybrid Non-Disjunction	5.90	0.56	0.4595	2.6/1.8
Monohybrid Justification	4.16	1.96	0.1698	3.7/3.1
Dihybrid Justification	4.91	1.59	0.2145	2.4/1.7
Monohybrid Problem	11.66	2.90	0.0972	14.8/13.8
Dihybrid Problem	3.33	0.25	0.6173	20.5/19.9
Definitions	2.15	0.69	0.4105	8.4/7.9
Relationships	4.00	1.04	0.3142	5.3/4.6

(I/NI) = Integrated vs. Non-integrated

The subjects in the integrated groups scored significantly higher on the test as a whole than did those in the non-integrated groups. In fact, the subjects from the integrated groups scored higher on each task, and in two cases the difference in scores was statistically significant. A discussion of the integration variable's effect on the task scores is presented below.

As can be seen in Table 9, the subjects who interacted with the integrated tutorials scored significantly higher on the trihybrid justification problem than did subjects from the non-integrated groups. This meant that once they had assigned alleles to gametes the integrated subjects were more likely to correctly use meiosis as the rationale for that assignment. This result is especially interesting because trihybrids were not discussed in the tutorials. Apparently, the integrated instruction allowed the subjects to more easily use meiosis in this new genetic situation.

The trihybrid justification task was but one which involved three pairs of genes. It was preceded by another which simply required subjects to assign alleles to the trihybrid's gametes. Regardless of instructional treatment, the subjects did very well on the assignment task, scoring an overall average of 1.85 out of the 2 possible points. The combined trihybrid gamete results indicate that in such situations some students who are able to generate correct answers cannot explain, in biological terms, why they are correct. This is similar to Stewart's (1982, 1983) findings with high school students.

The aneuploid gamete problem represented another novel genetic problem solving situation in which the integrated subjects fared significantly better. The integrated subjects scored higher on this task because they were more likely to use non-disjunction to explain the result or use a proper meiosis to show what was wrong. As with the trihybrid gamete problem, the integrated instruction appeared to facilitate the use of meiosis in novel genetic

problems.

The dihybrid non-disjunction question was the last of the novel, meiotically-oriented genetics problems. The integrated subjects again scored higher on this problem than did their non-integrated counterparts, but the difference was not statistically significant.

Although the integrated approach seemed to help with some new genetic situations, it made no statistically significant difference in familiar contexts. Subjects from all groups did equally well in offering sound meiotic justifications for their assignment of alleles to gametes in the monohybrid and dihybrid problems, which were similar to problems found in the tutorials. This result was unexpected and may be due to two factors. First, in the non-integrated tutorials the presentation of genetics followed meiosis by mere seconds. Perhaps this compact presentation allowed the subjects to appreciate the role of meiosis in contexts like those presented in the tutorials. Second, the genetic portions of all tutorials showed genes on chromosomes. It is possible that this image, repeated as it was many times, served to link meiosis and genetics for the type of familiar situations outlined above.

The monohybrid and dihybrid problems asked subjects to assign parental alleles to gametes, symbolically combine the gametes to produce zygotes, assign phenotypes to zygotic genotypes and determine phenotypic ratios. The integration variable might have played a role in the first task, assigning alleles to gametes. However, as outlined above, the subjects apparently had a good grasp of the biological mechanism of allele assortment in monohybrid and dihybrid contexts, so they rarely made mistakes at this point. Once the gametic genetic composition was determined, the remainder of either problem was apparently equally easy (or difficult) for all subjects to complete.

The criterion questions discussed thus far measured achievement using tasks which focused on the mechanisms of gametogenesis and inheritance. The criterion test measured achievement in other ways as well. One of those ways was to gauge how well the subjects could state relationships between genetics terms. Stewart (1982) identified some particularly difficult relationships during his interactions with high school students, and three of these (i.e. zygote-allele, allele-trait and gene-trait) appeared on the achievement test. The five other pairs of terms which appeared on the test represented troublesome relationships discussed by Cho, Kahle and Nordland (1985). As can be seen in Table 9, the integration variable had no significant differential impact on the subjects' performance of the relationships task. Perhaps the meiotic and problem-solving focus of the integration variable prevented it from having much effect. The same may also be true for the definitions task.

Sequence Variable

The expectations concerning the influence of the sequence variable were different than those associated with integration variable. Because the sequences used in this study had little to do with showing how meiosis and genetics were related, it was considered unlikely that sequence would have much impact on the "integration tasks" described in Table 8. Because the differences in sequence were centered in the monohybrid portions of the tutorials, it was thought some sequence effect might be measured by the monohybrid problem. Finally, it was uncertain whether any sequence effect would be detected by the dihybrid problem, the trihybrid gamete problem, or the concept relations task.

As shown in Table 10, and true to expectations, no effect of the sequence variable was detected by the "integration tasks".

Table 10
Summary of ANOVA Results and Means for SEQUENCE VARIABLE

TASK	MS	F(1,37)	p	MEANS (T/NT)
Test Overall	4.86	0.05	0.8237	58.8/58.3
Monohybrid Justification	0.54	0.25	0.6183	3.5/3.2
Dihybrid Justification	6.59	2.14	0.1519	2.5/1.7
Trihybrid Justification	0.05	0.03	0.8708	0.9/1.0
Aneuploid Gamete	0.23	0.29	0.5912	0.55/0.71
Dihybrid Non-Disjunction	18.58	1.76	0.1929	2.85/1.52
Monohybrid Problem	19.36	4.81	0.0347*	13.6/14.9
Dihybrid Problem	14.63	1.11	0.2979	19.6/20.8
Trihybrid Gametes	0.09	0.30	0.5882	1.9/1.8
Definitions	13.34	4.30	0.0452*	8.7/7.6
Relationships	0.18	0.05	0.8286	4.9/5.0

(T/NT) = Tolman vs. Non-Tolman sequence

Expectations were further borne out by the results of the monohybrid problem (see Table 10). In this case subjects who experienced the traditional (autosomal-inheritance-first) sequence scored significantly higher than did those from the Tolman sequence (sex-linked-inheritance-first) groups. This result may be explained theoretically in either or both of two ways. Ausubelian (Ausubel, Novak & Hanesian, 1978) theory argues that instructional sequences should begin with general principles and then proceed to more specific ones. The traditional sequence conformed to this rule by presenting the general principles of autosomal inheritance first, followed by the specific principles associated with sex-linked inheritance. The traditional sequence also conformed to the widely applied maxim that instructional sequences should begin with simple ideas and then move on to more complex ones. (Sex-linkage adds a layer of complexity because it requires one to keep track of specific chromosomes as well as genes.) In short, the traditional sequence embraced two theoretically sound approaches, either one or both of which could have promoted the learning which lead to the performance difference.

As outlined above, it was difficult to predict what effect the sequence variable would have on the dihybrid and trihybrid problems. Apparently, the sequence variable had no effect, as shown in Table 10.

The sequence variable did have an effect on the definitions portion of the concept relations task, as can be seen in Table 10. Subjects who experienced the Tolman sequence scored significantly higher on this task than did those from the traditional sequence groups. This is rather curious because contextual differences (i.e. examples used in the tutorials to illustrate the meanings of the terms) cannot fully explain the difference in performance. One subset of five terms found in the definitions task were

defined using different examples, as dictated by the sequence variable. However, the other five were defined in precisely the same way. Interestingly, the subjects from the Tolman groups were more likely to correctly define terms from both subsets. Contextual differences might explain the disparity in performance for terms in the first subset, but what of those defined in the common way? Barring chance, this outcome eludes full explanation.

Finally, the sequence variable had no detectable effect on the outcome of the relationships task. This may mean, in light of the definitions result, that knowledge of the definitions of terms does not necessarily imply knowledge of their interrelationships.

CONCLUSIONS

In this study the integrated approach to teaching meiosis and genetics stressed gene-chromosome relationships, the importance of meiosis in determining the genetic composition of parental gametes, and the biological meanings of the symbols used in Punnett squares. When measured by the instrument developed by the investigator for this study, the pattern of results obtained from 41, college, introductory biology students who received computer-delivered instruction indicate that the integrated approach tends to promote higher achievement in genetics than the non-integrated approach. This conclusion is warranted because: the integrated subjects total achievement scores were significantly higher than those of the non-integrated subjects; the integrated subjects scored significantly higher on two, novel genetics problems; and, although not statistically significant, the integrated subjects outscored their non-integrated counterparts on the remaining eight achievement tasks.

This study also measured the effects of two different instructional sequences on the genetics achievement of college, introductory biology students. One sequence, devised by Tolman (1982), discussed single gene pair sex-linkage and monohybrid autosomal patterns of inheritance in that order; the other, considered more traditional, was the reverse. The overall effect of sequence is difficult to assess, considering the general lack of pattern in the results and the conflict between the outcomes of the monohybrid problem (which favored the traditional sequence) and definitions task (which favored the Tolman sequence). It is perhaps safe to say that at the college level this study does not provide enough evidence to warrant the abandonment of the traditional sequence for that described by Tolman.

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Appendix A

The Criterion Test and Scoring Key

Concepts and their relationships

Part A - definitions (Each definition was worth one point.)

Please define each term below in one or two sentences.

1) allele	A particular form of a gene.
2) chromosome	A complex structure composed of proteins and DNA that carry hereditary data.
3) DNA	A nucleic acid that carries hereditary information capable of duplication and directing the metabolism of the cell.
4) gamete	A haploid reproductive cell.
5) gene	A unit of heredity that interacts with the environment to control the expression of a given trait.
6) heterozygous	In a diploid organism, the state of having two different alleles in a given gene pair.
7) homologue	One of a pair of chromosomes carrying genes controlling the expression of the same traits.
8) homozygous	In a diploid organism, the state of having identical alleles in a given gene pair.
9) trait	A general characteristic of an organism, eg. eye color, beta-globin production, etc. (A general term, more global than form or variety.)
10) zygote	The single-celled entity created when an egg is fertilized by a sperm.

Part B - relationships (Each relationship was worth one point.)

Below you will find pairs of terms. For each pair, please state in one or two sentences a relationship that exists between the terms.

Example: nucleus/chromosome

The nucleus is a cellular organelle that contains the chromosomes when cell division is not underway.

1) gene/DNA	A gene is a specific segment of DNA.
2) gene/chromosome	Genes are arranged linearly along a chromosome.
3) trait/allele	An allele is responsible for the expression of a specific form (or variation of a trait.
4) gamete/homologue	Each gamete should contain one homologue from each pair of homologues present in the cell that gave rise to the gamete.
5) gamete/allele	Each gamete should contain one allele from each pair of alleles present in the cell that gave rise to the gamete.
6) zygote/homologue	A zygote should contain homologous chromosomes in pairs.
7) zygote/allele	A zygote should contain a pair of alleles for each gene.
8) trait/gene	In most cases, a pair of genes, in form or another, controls the expression of a given trait.

3) It is possible to inherit a dominant allele that causes one to have extra fingers and toes, a condition called polydactyly. Suppose a woman who has 12 fingers marries a man who also has extra digits. They plan to have children. The genotypes of these people with respect to this gene pair are:

Pp	Pp
mother	father

Answer the following: (When representing genes, please underline all lower case letters.)

a) In terms of the genes above, what are the possible eggs of the mother?

Correct answer: P and p. Point value: 2.

b) In terms of the genes above, what are the possible sperm of the father?

Correct answer: P and p. Point value: 2.

c) Explain in detail how you determined what the genetic composition of the sperm of the father would be. Use any diagram(s) and/or rule(s) you feel are necessary. (Use the back, if necessary.)

Correct meiotic explanations or diagrams - 4 points. Mention of meiosis, but no details - 1 point.

d) Show the genotypes of all possible zygotes that could result from these parents.

Correct answer: PP, Pp, and pp. Point value: 3.

e) Show the phenotype associated with each genotype in question (d) above. Explain how you determined each phenotype.

Correct answer:
PP - polydactyly - dominant allele effect.
Pp - polydactyly - dominant allele masks recessive.
pp - normal numbers of digits - recessive allele effect.

Point value: one point for each phenotype and one point for each correct explanation for a total of 6 points.

f) Show the ratio of the phenotypes of the offspring.

Correct answer: 3:1 polydactyly:normal. Point value: 1.

g) Suppose the parents above plan to have 100 children, and they ask you to predict the phenotypes of their offspring with respect to the trait of polydactyly. What would be your best guess? EXPLAIN YOUR ANSWER.

Correct answer: About 75 with polydactyly, 25 without. Also something must be said concerning the probabilistic nature of the prediction.

Point value: 2.

4) A woman who has normal hemoglobin production and will be afflicted with Huntington's Disease marries and has children with a man who carries the recessive beta-thalassemia allele and will also face Huntington's Disease. The following are their genotypes:

TTHh	TtHh
mother	father

Answer the following: (When representing genes, please underline all lower case letters.)

a) In terms of the genes above, what are the possible eggs of the mother?

Correct answer: TH and Th. Point value: 2.

b) In terms of the genes above, what are the possible sperm of the father?

Correct answer: TH, Th, tH, and th. Point value: 4.

c) Explain in detail how you determined what the genetic composition of the eggs of the mother would be. Use any diagram(s) and/or rule(s) you feel are necessary. (Use the back, if necessary.)

Correct meiotic explanations or diagrams - 4 points. Mention of meiosis, but no details - 1 point.

d) Show the genotypes of all possible zygotes that could result from these parents.

Correct answer: (See question e). Point value: 8.

e) Show the phenotype associated with each genotype in question (d) above.

Correct answer:

Genotype	Phenotype
TTHH	HD*, No BT*
TTHh	HD, No BT
TtHH	HD, No BT
TtHh	HD, No BT
TTHh	HD, No BT
TThh	No HD, No BT
TtHh	HD, No BT
Tthh	No HD, No BT

*HD - Huntington's Disease BT - Beta-thalassemia

Point value: 8.

f) Show the ratio of the phenotypes of the offspring.

Correct Answer: 3:1 Huntington's Disease to No Huntington's Disease. (All offspring escape beta-thalassemia.)

Point Value: 1.

5) A woman who is Rh positive, a carrier of the beta-thalassemia recessive allele and has Huntington's Disease marries and has children with a man who is Rh positive, a carrier of the beta-thalassemia recessive allele and normal with respect to Huntington's Disease. The genotypes of the parents are:

RrTtHh	RRTthh
mother	father

Answer the following: (When representing genes, please underline all lower case letters.)

a) In terms of the genes above, what are the possible sperm of the father?

Correct answer: RTh and Rth. Point value: 2.

b) Explain in detail how you determined what the genetic composition of the sperm of the father would be. Use any diagram(s) and/or rule(s) you feel are necessary. (Use the back, if necessary.)

Correct meiotic explanations or diagrams - 4 points. Mention of meiosis, but no details - 1 point.
Showed correct meiosis with genes linked - 1 point.

6) Suppose a person has the following genotype with respect to one of his/her gene pairs: Aa.

Suppose the following is the genetic composition of one of his/her gametes: Aa.

Could such a gamete be produced by this person? Explain why or why not.

Answered yes and showed proper non-disjunction - 4 pts.
Answered yes, but only generally discussed non-disjunction - 2 pts.
Answered no and showed proper meiosis as explanation - 1 pt.

7) The genes controlling the expression of the Rh blood type are found on chromosome pair #1 in humans. The genes controlling the onset of Huntington's Disease are found on chromosome pair #4.

The following is the genotype of an individual who has Rh positive blood and will develop Huntington's Disease: RrHh. Using the RrHh individual just described, assume the following: this person is male and during one meiosis the homologous chromosomes of pair #1 fail to separate. Indicate below the genetic composition of the sperm that would result from such an occurrence in a single meiosis. EXPLAIN YOUR ANSWER. Use whatever diagrams you feel are necessary.

Each correct gamete (four altogether): 1 point.
Showed non-disjunction in first meiosis : 4 points.
Showed non-disjunction in second meioss : 2 points.
(Non-disjunction points were mutually exclusive.)
Total points possible on question #7: 8.